

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 6,893,636 B2
DATED : May 17, 2005
INVENTOR(S) : Reff et al.

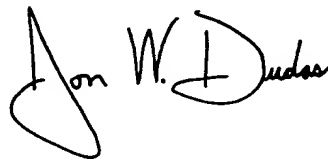
Page 1 of 30

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Delete Columns 47-64 and Columns 65-66, lines 1-42 and insert the attached pages.

Signed and Sealed this

Ninth Day of May, 2006

A handwritten signature in black ink, reading "Jon W. Dudas". The signature is stylized, with a large loop for the "J" and a cursive "Dudas".

JON W. DUDAS
Director of the United States Patent and Trademark Office

SEQUENCE LISTING

<110> REFF, MITCHELL E.
KLOETZER, WILLIAM S.
NAKAMURA, TAKEHIKO

<120> GAMMA-1 AND GAMMA-3 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
THEREOF AS THERAPEUTICS

<130> 037003-0275470

<140> 09/019,441

<141> 1998-02-05

<150> 08/803,085

<151> 1997-02-20

<160> 39

<170> PatentIn Ver. 2.1

<210> 1

<211> 390

<212> DNA

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<223> Description of Artificial Sequence: Mature peptide is derived from Old
World Monkey (macaque); leader sequence is an artificial sequence to
facilitate cloning

<220>

<221> misc_feature

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<223> leader sequence

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<222> (58)..(390)

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tcc tgg gct cag tct gcc ccg act cag cct ccc tct gtg tct ggg tct	96
Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser	
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cct gga cag tcg gtc acc atc tcc tgc act gga acc agc gat gac gtt	144
Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val	
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ggt ggt tat aac tat gtc tcc tgg tac caa cac cac cca ggc aaa gcc 192
 Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His Pro Gly Lys Ala
 30 35 40 45

ccc aaa ctc atg att tat gat gtc gct aag cgg gcc tca ggg gtc tct 240
 Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser
 50 55 60

gat cgc ttc tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc 288
 Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
 65 70 75

tct ggg ctc cag gct gag gac gag gct gat tat tac tgt tgt tca tat 336
 Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr
 80 85 90

aca acc agt agc act ttg tta ttc gga aga ggg acc cgg ttg acc gtc 384
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 Leu Gly
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Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val
 15 20 25

Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala
 30 35 40 45

Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser
 50 55 60

Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
 65 70 75

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 80 85 90

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Leu Gly
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<222> (1)..(423)

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gtc ctg tcc cag ctg cag ctg cag gag tgc ggc cca gga gtg gtg aag	96
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cct tgc gag acc ctg tcc ctc acc tgc gct gtc tct ggt ggc tct gtc	144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val	
15 20 25	
agc agt agt aac tgg tgg acc tgg atc cgc cag ccc cca ggg aag gga	192
Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly	
30 35 40 45	
ctg gag tgg att gga cgt atc tct ggt agt ggt ggg gcc acc aac tac	240
Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr	
50 55 60	
aac ccg tcc ctc aag agt cga gtc atc att tca caa gac acg tcc aag	288
Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys	
65 70 75	
aac cag ttc tcc ctg aac ctg aac tct gtg acc gcc gcg gac acg gcc	336
Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala	
80 85 90	
gtg tat tac tgt gcc aga gat tgg gcc caa ata gct gga aca acg cta	384
Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu	
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Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly
 30 35 40 45

Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr
 50 55 60

Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys
 65 70 75

Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala
 80 85 90

Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu
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Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser
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ctc cca ggt gcc aga tgt gac atc cag atg acc cag tct cca tct tcc 96
Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
      -5          -1 1          5          10

ctg tct gca tct gta ggg gac aga gtc acc atc act tgc agg gca agt 144
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
          15          20          25

cag gac att agg tat tat tta aat tgg tat cag cag aaa cca gga aaa 192
Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
          30          35          40

gct cct aag ctc ctg atc tat gtt gca tcc agt ttg caa agt ggg gtc 240
Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
          45          50          55

cca tca agg ttc agc ggc agt gga tct ggg aca gag ttc act ctc acc 288
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
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gtc agc agc ctg cag cct gaa gat ttt gcg act tat tac tgt cta cag 336
Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
          75          80          85          90

gtt tat agt acc cct cgg acg ttc ggc caa ggg acc aag gtg gaa atc 384
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aaa 387
Lys

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      30           35           40
Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
      45           50           55
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
      60           65           70
Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
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Lys

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gtc cag tgt gag gtg cag ctg gtg gag tct ggg ggc ggc ttg gca aag 96
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Lys
      -1  1           5           10
cct ggg ggg tcc ctg aga ctc tcc tgc gca gcc tcc ggg ttc agg ttc 144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe
      15           20           25

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acc ttc aat aac tac tac atg gac tgg gtc cgc cag gct cca ggg cag 192
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ggg ctg gag tgg gtc tca cgt att agt agt agt ggt gat ccc aca tgg 240
 Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Ser Gly Asp Pro Thr Trp
 50 55 60

tac gca gac tcc gtg aag ggc aga ttc acc atc tcc aga gag aac gcc 288
 Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala
 65 70 75

aac aac aca ctg ttt ctt caa atg aac agc ctg aga gct gag gac acg 336
 Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 80 85 90

gct gtc tat tac tgt gcg agc ttg act aca ggg tct gac tcc tgg ggc 384
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Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Lys
 -1 1 5 10

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe
 15 20 25

Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln
 30 35 40 45

Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Ser Gly Asp Pro Thr Trp
 50 55 60

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala
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Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
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SEQUENCE LISTING

<110> REFF, MITCHELL E.
KLOETZER, WILLIAM S.
NAKAMURA, TAKEHIKO

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THEREOF AS THERAPEUTICS

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<160> 39

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tcc tgg gct cag tct gcc ccg act cag cct ccc tct gtg tct ggg tct	96
Ser Trp Ala Gln Ser Ala Pro Thr Gln Pro Pro Ser Val Ser Gly Ser	
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cct gga cag tcg gtc acc atc tcc tgc act gga acc agc gat gac gtt	144
Pro Gly Gln Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Asp Asp Val	
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 30 35 40 45

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 50 55 60

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 Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
 65 70 75

tct ggg ctc cag gct gag gac gag gct gat tat tac tgt tgt tca tat 336
 Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr
 80 85 90

aca acc agt agc act ttg tta ttc gga aga ggg acc cgg ttg acc gtc 384
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cta ggt 390
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 -1 1 5 10

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 15 20 25

Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln His His Pro Gly Lys Ala
 30 35 40 45

Pro Lys Leu Met Ile Tyr Asp Val Ala Lys Arg Ala Ser Gly Val Ser
 50 55 60

Asp Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile
 65 70 75

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Leu Gly
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Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp	
-15 -10 -5	
gtc ctg tcc cag ctg cag ctg cag gag tgc ggc cca gga gtg gtg aag	96
Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys	
-1 1 5 10	
cct tgc gag acc ctg tcc ctc acc tgc gct gtc tct ggt ggc tct gtc	144
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val	
15 20 25	
agc agt agt aac tgg tgg acc tgg atc cgc cag ccc cca ggg aag gga	192
Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly	
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ctg gag tgg att gga cgt atc tct ggt agt ggt ggg gcc acc aac tac	240
Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr	
50 55 60	
aac ccg tcc ctc aag agt cga gtc atc att tca caa gac acg tcc aag	288
Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys	
65 70 75	
aac cag ttc tcc ctg aac ctg aac tct gtg acc gcc gcg gac acg gcc	336
Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala	
80 85 90	
gtg tat tac tgt gcc aga gat tgg gcc caa ata gct gga aca acg cta	384
Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu	
95 100 105	

ggc ttc tgg ggc cag gga gtc ctg gtc acc gtc tcc tca 423
 Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser
 110 115 120

<210> 4
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

<400> 4

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 -15 -10 -5

Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Val Val Lys
 -1 1 5 10

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Val
 15 20 25

Ser Ser Ser Asn Trp Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly
 30 35 40 45

Leu Glu Trp Ile Gly Arg Ile Ser Gly Ser Gly Gly Ala Thr Asn Tyr
 50 55 60

Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser Gln Asp Thr Ser Lys
 65 70 75

Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala
 80 85 90

Val Tyr Tyr Cys Ala Arg Asp Trp Ala Gln Ile Ala Gly Thr Thr Leu
 95 100 105

Gly Phe Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser
 110 115 120

<210> 5
 <211> 387
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

<220>
 <221> misc_feature
 <222> (1)..(66)
 <223> leader sequence

<220>

<221> mat_peptide

<222> (67)..(387)

<220>

<221> CDS

<222> (1)..(387)

<400> 5

atg gac atg agg gtc ccc gct cag ctc ctg ggg ctc ctt ctg ctc tgg	48
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp	
-20 -15 -10	
ctc cca ggt gcc aga tgt gac atc cag atg acc cag tct cca tct tcc	96
Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser	
-5 -1 1 5 10	
ctg tct gca tct gta ggg gac aga gtc acc atc act tgc agg gca agt	144
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser	
15 20 25	
cag gac att agg tat tat tta aat tgg tat cag cag aaa cca gga aaa	192
Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys	
30 35 40	
gct cct aag ctc ctg atc tat gtt gca tcc agt ttg caa agt ggg gtc	240
Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val	
45 50 55	
cca tca agg ttc agc ggc agt gga tct ggg aca gag ttc act ctc acc	288
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr	
60 65 70	
gtc agc agc ctg cag cct gaa gat ttt gcg act tat tac tgt cta cag	336
Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln	
75 80 85 90	
gtt tat agt acc cct cgg acg ttc ggc caa ggg acc aag gtg gaa atc	384
Val Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile	
95 100 105	
aaa	387
Lys	

<210> 6

<211> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

<400> 6

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp
-20 -15 -10
Leu Pro Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser

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      -5          -1   1          5          10
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
              15              20              25
Gln Asp Ile Arg Tyr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
              30              35              40
Ala Pro Lys Leu Leu Ile Tyr Val Ala Ser Ser Leu Gln Ser Gly Val
              45              50              55
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
              60              65              70
Val Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
              75              80              85              90
Val Tyr Ser Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
              95              100              105

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Lys

<210> 7

<211> 411

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

<220>

<221> misc_feature

<222> (1)..(57)

<223> leader sequence

<220>

<221> mat_peptide

<222> (58)..(411)

<220>

<221> CDS

<222> (1)..(411)

<400> 7

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atg gag ttt ggg ctg agc tgg gtt ttc ctt gtt cct ctt ttg aaa ggt      48
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Pro Leu Leu Lys Gly
              -15              -10              -5

gtc cag tgt gag gtg cag ctg gtg gag tct ggg ggc ggc ttg gca aag      96
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Lys
              -1   1              5              10

cct ggg ggg tcc ctg aga ctc tcc tgc gca gcc tcc ggg ttc agg ttc      144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe
              15              20              25

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acc ttc aat aac tac tac atg gac tgg gtc cgc cag gct cca ggg cag 192
 Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln
 30 35 40 45

ggg ctg gag tgg gtc tca cgt att agt agt agt ggt gat ccc aca tgg 240
 Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Ser Gly Asp Pro Thr Trp
 50 55 60

tac gca gac tcc gtg aag ggc aga ttc acc atc tcc aga gag aac gcc 288
 Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala
 65 70 75

aac aac aca ctg ttt ctt caa atg aac agc ctg aga gct gag gac acg 336
 Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 80 85 90

gct gtc tat tac tgt gcg agc ttg act aca ggg tct gac tcc tgg ggc 384
 Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly
 95 100 105

cag gga gtc ctg gtc acc gtc tcc tca 411
 Gln Gly Val Leu Val Thr Val Ser Ser
 110 115

<210> 8

<211> 137

<212> PRT

<213> Artifical Sequence

<220>

<223> Description of Artificial Sequence: Mature peptide is derived from Old World Monkey (macaque); leader sequence is an artificial sequence to facilitate cloning

<400> 8

Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Pro Leu Leu Lys Gly
 -15 -10 -5

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ala Lys
 -1 1 5 10

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Arg Phe
 15 20 25

Thr Phe Asn Asn Tyr Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Gln
 30 35 40 45

Gly Leu Glu Trp Val Ser Arg Ile Ser Ser Ser Gly Asp Pro Thr Trp
 50 55 60

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Glu Asn Ala
 65 70 75

Asn Asn Thr Leu Phe Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 80 85 90

Ala Val Tyr Tyr Cys Ala Ser Leu Thr Thr Gly Ser Asp Ser Trp Gly
 95 100 105

Gln Gly Val Leu Val Thr Val Ser Ser
110 115

<210> 9

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 9

atcacagatc tctcaccatg gacatgaggg tccccgctca g 41

<210> 10

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 10

atcacagatc tctcaccatg aggctccctg ctca 35

<210> 11

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 11

atcacagatc tctcaccatg gaarccccag ckca 35

<210> 12

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 12

atcacagatc tctcaccatg gtgttgcaga cccaggtc 38

<210> 13

<211> 32

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 13

ggtgcagcca ccgtagcttt gatytcasc tt 32

<210> 14
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 14

atcacagatc tctcaccatg rcctgstccc ctct 34

<210> 15
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 15

atcacagatc tctcaccatg gcctggctc ygct 34

<210> 16
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 16
 atcacagatc tctcaccatg gcmtggaycc ctctc 35

<210> 17
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 17

cttgggctga cctaggacgg t 21

<210> 18
 <211> 30

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 18

gcgactaagt cgaccatgga ctggacctgg 30

<210> 19
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 19

gcgactaagt cgaccatgaa acacctgtgg 30

<210> 20
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 20

gcgactaagt cgaccatgga gtttgggctg agc 33

<210> 21
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 21

gcgactaagt cgaccatggg gtcaaccgcc atc 33

<210> 22
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 22

gcgactaagt cgaccatgtc tgtctccttc etc 33

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<210> 23
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23

gccaggggga agaccgatgg gcccttggtg ctagctgagg agacgg 46

<210> 24
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24

gatgggccct tggtagtagc tgaggagacg g 31

<210> 25
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25

ggtgctagct gaggagacgg tgaccaggac tccctggccc cagaagccta g 51

<210> 26
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26

atttaggtga cactata 17

<210> 27
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27

gttttcccag tcacga

16

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 28

atatacgact cactataggg

20

<210> 29

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 29

ccgtcagatc gcctggagac gcc

24

<210> 30

<211> 20

<212> DNA

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<220>

<223> Description of Artificial Sequence: Primer

<400> 30

gcagttccag atttcaactg

20

<210> 31

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 31

ccaggccact gtcacggctt c

21

<210> 32

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 32

cagagctggg tacgtcctca

20

<210> 33

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 33

gccccagag gtgctcttg

20

<210> 34

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 34

acacagacc gtcgacatg

20

<210> 35

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 35

gctctcggag gtgctcctg

20

<210> 36

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 36

acagaccgt cgaccatgga gtttgggctg

30

<210> 37
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 37

ccccttggtg ctagctgagg agacggt 27

<210> 38
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 38

agagagaacg ccaagaacac actgttt 27

<210> 39
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 39

aaacagtgtg ttcttggcgt tctctct 27